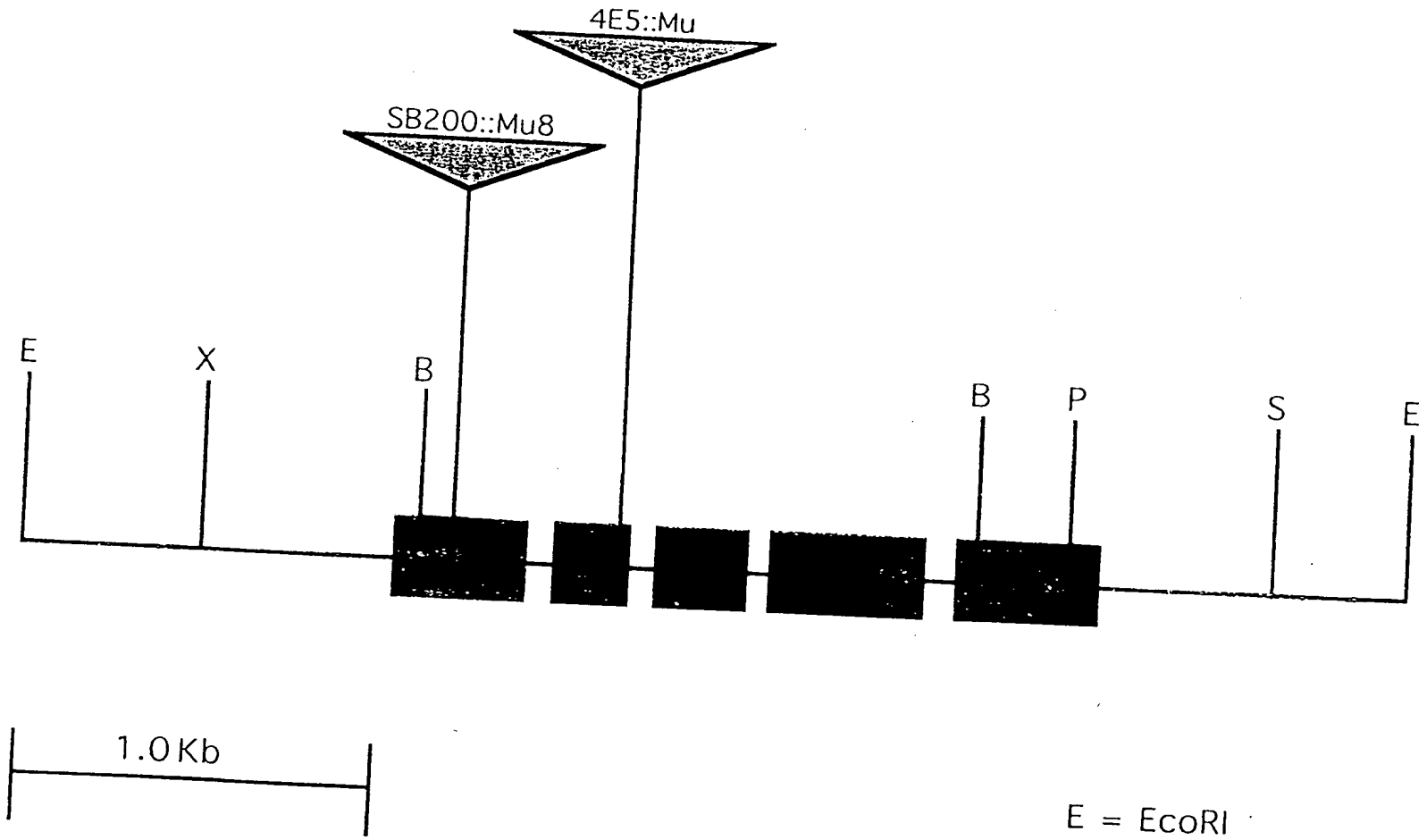
4E5::Mu
SB200::Mu8
E
X
B
B
P
S
E
1.0Kb
E = EcoRI
X = XbaI
B = BamHI
P = PstI
S = SacI

FIGURE 1

TOHTZT" 4591200T

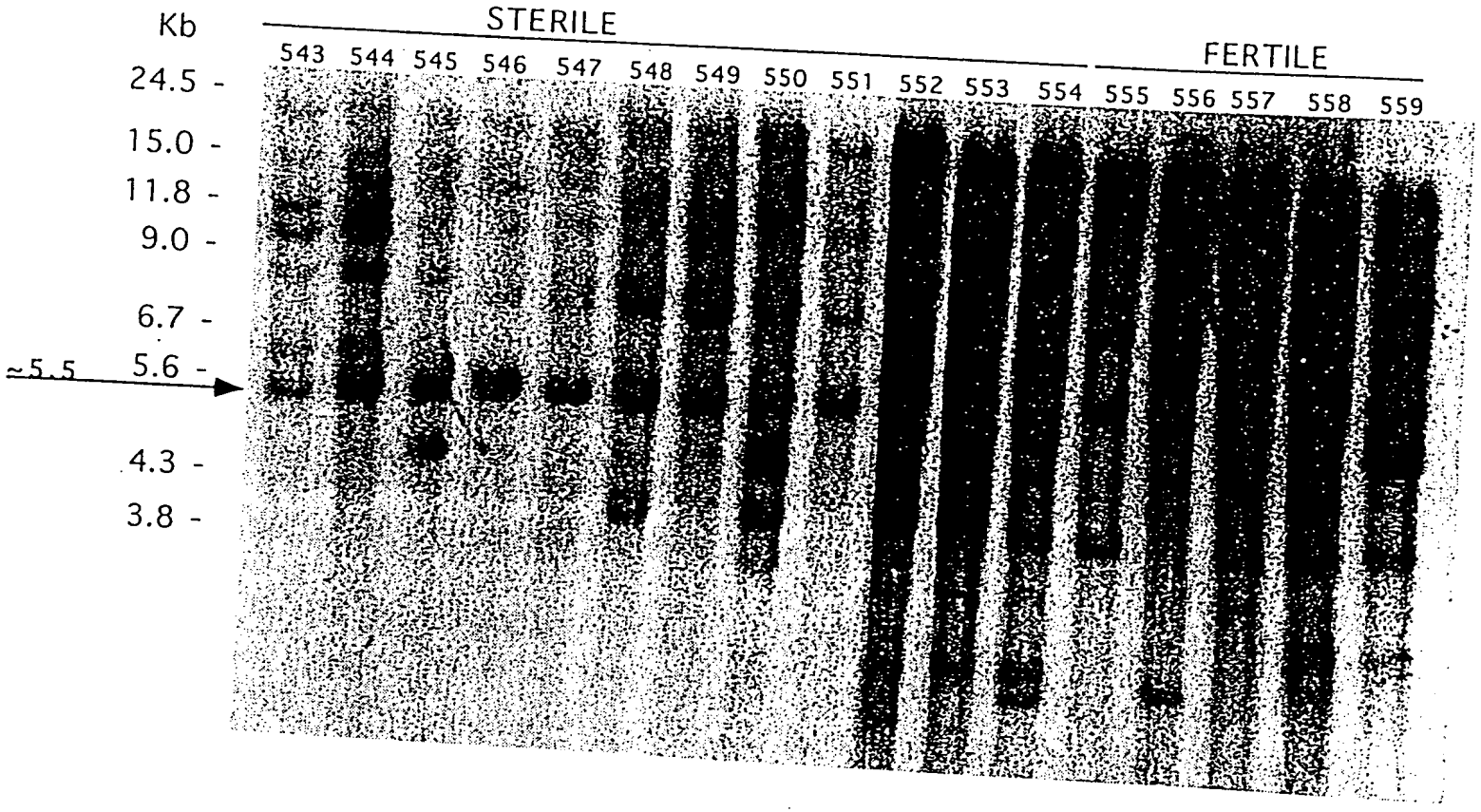

FIGURE 2

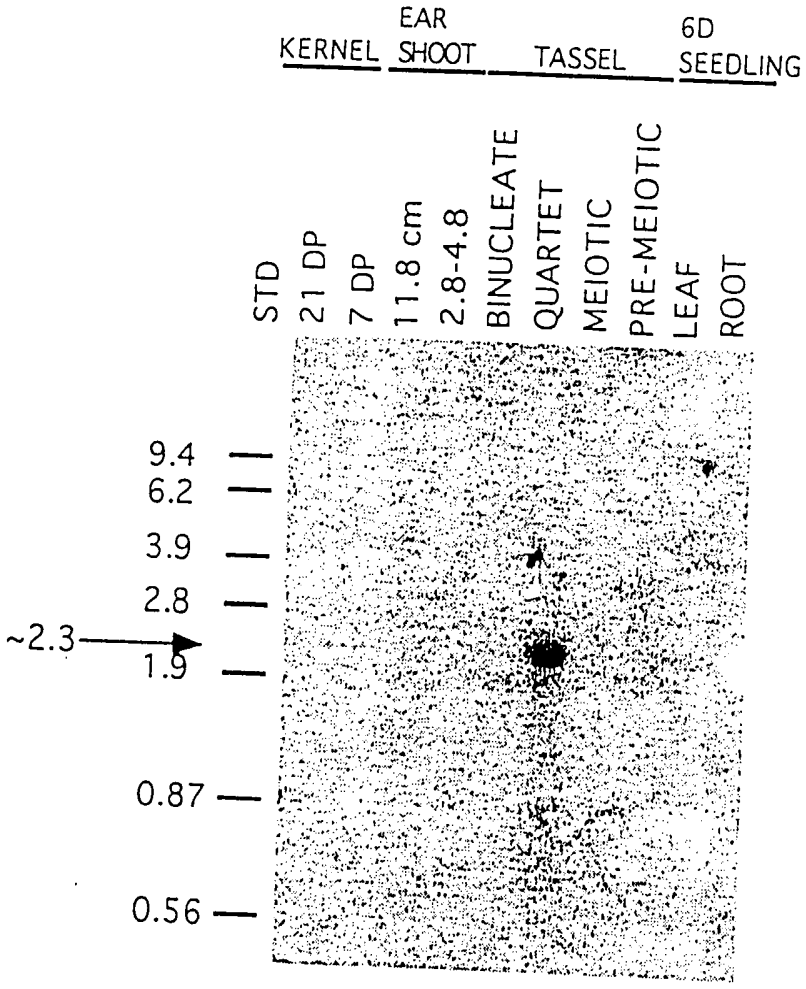
KERNEL
EAR SHOOT
TASSEL
6D SEEDLING
STD
21 DP
7 DP
11.8 cm
2.8-4.8
BINUCLEATE
QUARTET
MEIOTIC
PRE-MEIOTIC
LEAF
ROOT
9.4
6.2
3.9
2.8
~2.3
1.9
0.87
0.56

FIGURE 3

Figure 4

```
   EcoRI
     |
     GAATTCGGCACGAGGGAAGCTCACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTA
   1 ---------+---------+---------+---------+---------+---------+ 60
     CTTAAGCCGTGCTCCCTTCGAGTGGAGTGCGGCCGCTGCGGTAGCGGTAAGAAGGGTGAT

a     E  F  G  T  R  E  A  H  L  T  P  A  T  P  S  P  F  F  P  L  -

     GCAGGGCCTCACAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAG
  61 ---------+---------+---------+---------+---------+---------+ 120
     CGTCCCGGAGTGTTCATGTAGCGCGAGGAAGACCAACAGGAGAGTACCTAGGACCAGGTC

a     A  G  P  H  K  Y  I  A  L  L  L  V  V  L  S  W  I  L  V  Q  -

     AGGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGCGCAACGGTG
 121 ---------+---------+---------+---------+---------+---------+ 180
     TCCACCTCGGACTCCTTCGTCTTTCCGGGCTCTAGTACCGGTCAGTAGCCGCGTTGCCAC

a     R  W  S  L  R  K  Q  K  G  P  R  S  W  P  V  I  G  A  T  V  -

     GAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGTCGGGTACCTGTCACGGCAC
 181 ---------+---------+---------+---------+---------+---------+ 240
     CTCGTCGACTCCTTGATGGTGGCCTACGTGCTGACCGAACAGCCCATGGACAGTGCCGTG

a     E  Q  L  R  N  Y  H  R  M  H  D  W  L  V  G  Y  L  S  R  H  -

     AGGACAGTGACCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT
 241 ---------+---------+---------+---------+---------+---------+ 300
     TCCTGTCACTGGCAGCTGTACGGCAAGTGAAGGATGTGGATGTAGCGACTGGGCCACTTA

a     R  T  V  T  V  D  M  P  F  T  S  Y  T  Y  I  A  D  P  V  N  -

     GTCGAGCATGTCCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGTGTACAGATCC
 301 ---------+---------+---------+---------+---------+---------+ 360
     CAGCTCGTACAGGAGTTCTGATTGAAGTGGTTAATGGGGTTCCCTTAGCACATGTCTAGG

a     V  E  H  V  L  K  T  N  F  T  N  Y  P  K  G  I  V  Y  R  S  -

     TACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCGACGGCGAGCTGTGGAGGAAG
 361 ---------+---------+---------+---------+---------+---------+ 420
     ATGTACCTGCACGAGGAGCCACTGCCGTAGAAGTTGCGGCTGCCGCTCGACACCTCCTTC

a     Y  M  D  V  L  L  G  D  G  I  F  N  A  D  G  E  L  W  R  K  -

     CAGAGGAAGACGGCGAGTTTCGAGTTCGCCTCCAAGAACCTGAGGGATTTCAGCGCCATT
 421 ---------+---------+---------+---------+---------+---------+ 480
     GTCTCCTTCTGCCGCTCAAAGCTCAAGCGGAGGTTCTTGGACTCCCTAAAGTCGCGGTAA

a     Q  R  K  T  A  S  F  E  F  A  S  K  N  L  R  D  F  S  A  I  -
```

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Figure 4B

```
        GTGTTCAGAGAGTACTCCCTGAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGGC
   481  ---------+---------+---------+---------+---------+---------+ 540
        CACAAGTCTCTCATGAGGGACTTCGACAGCCCATATGACTCGGTCCGTAGGTTCCGTCCG

a        V  F  R  E  Y  S  L  K  L  S  G  I  L  S  Q  A  S  K  A  G  -

        AAAGTTGTGGACATGCAGGAACTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT
   541  ---------+---------+---------+---------+---------+---------+ 600
        TTTCAACACCTGTACGTCCTTGAAATGTACTCCTACTGCGACCTGAGGTAGACGTTCCAA

a        K  V  V  D  M  Q  E  L  Y  M  R  M  T  L  D  S  I  C  K  V  -

        GGGTTCGGGGTCGAGATCGGCACGCTGTCGCCAGATCTCCCCGAGAACAGCTTCGCGCAG
   601  ---------+---------+---------+---------+---------+---------+ 660
        CCCAAGCCCCAGCTCTAGCCGTGCGACAGCGGTCTAGAGGGGCTCTTGTCGAAGCGCGTC

a        G  F  G  V  E  I  G  T  L  S  P  D  L  P  E  N  S  F  A  Q  -

        GCGTTCGATGCCGCCAACATCATCATCACGCTGCGGTTCATCGACCCGCTGTGGCGCATC
   661  ---------+---------+---------+---------+---------+---------+ 720
        CGCAAGCTACGGCGGTTGTAGTAGTAGTGCGACGCCAAGTAGCTGGGCGACACCGCGTAG

a        A  F  D  A  A  N  I  I  I  T  L  R  F  I  D  P  L  W  R  I  -

        AAGAGGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGAGCATCAAGCTCGTGGAC
   721  ---------+---------+---------+---------+---------+---------+ 780
        TTCTCCAAGAAGGTGCAGCCCAGTCTCCGGGAGGATCGCGTCTCGTAGTTCGAGCACCTG

a        K  R  F  F  H  V  G  S  E  A  L  L  A  Q  S  I  K  L  V  D  -

        GAGTTCACCTACAGCGTGATCCGCCGGAGGAAGGCCGAGATCGTCGAGGTCCGGGCCAGC
   781  ---------+---------+---------+---------+---------+---------+ 840
        CTCAAGTGGATGTCGCACTAGGCGGCCTCCTTCCGGCTCTAGCAGCTCCAGGCCCGGTCG

a        E  F  T  Y  S  V  I  R  R  R  K  A  E  I  V  E  V  R  A  S  -

        GGCAAACAGGAGAAGATGAAGCACGACATCCTGTCACGGTTCATCGAGCTGGGCGAGGCC
   841  ---------+---------+---------+---------+---------+---------+ 900
        CCGTTTGTCCTCTTCTACTTCGTGCTGTAGGACAGTGCCAAGTAGCTCGACCCGCTCCGG

a        G  K  Q  E  K  M  K  H  D  I  L  S  R  F  I  E  L  G  E  A  -

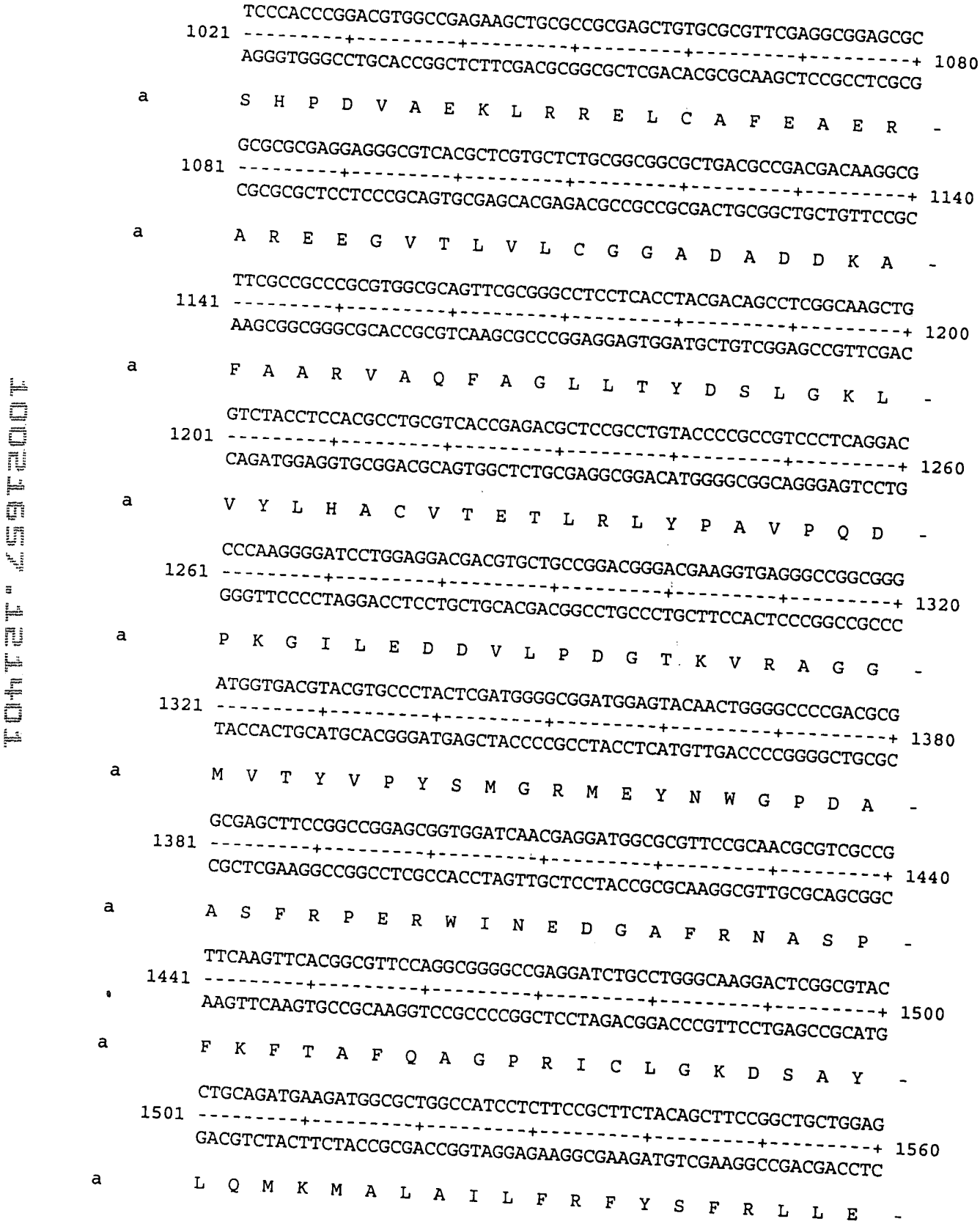
        GGCGACGACGGCGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTGCTCAACTTC
   901  ---------+---------+---------+---------+---------+---------+ 960
        CCGCTGCTGCCGCCGCCGAAGCCCCTGCTATTCTCGGAGGCCCTGCACCACGAGTTGAAG

a        G  D  D  G  G  G  F  G  D  D  K  S  L  R  D  V  V  L  N  F  -

        GTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCGTGGTTCACGCACATGGCCATG
   961  ---------+---------+---------+---------+---------+---------+ 1020
        CACTAGCGGCCCGCCCTGTGCTGCCGCTGCTGCGACAGCACCAAGTGCGTGTACCGGTAC

a        V  I  A  G  R  D  T  T  A  T  T  L  S  W  F  T  H  M  A  M  -
```

Figure 4C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1021
AGGGTGGGCCTGCACCGGCTCTTCGACGCGGCGCTCGACACGCGCAAGCTCCGCCTCGCG
1080
a S H P D V A E K L R R E L C A F E A E R -
GCGCGCGAGGAGGGCGTCACGCTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCG
1081
CGCGCGCTCCTCCCGCAGTGCGAGCACGAGACGCCGCCGCGACTGCGGCTGCTGTTCCGC
1140
a A R E E G V T L V L C G G A D A D D K A -
TTCGCCGCCCGCGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTG
1141
AAGCGGCGGGCGCACCGCGTCAAGCGCCCGGAGGAGTGGATGCTGTCGGAGCCGTTCGAC
1200
a F A A R V A Q F A G L L T Y D S L G K L -
GTCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTCCCTCAGGAC
1201
CAGATGGAGGTGCGGACGCAGTGGCTCTGCGAGGCGGACATGGGGCGGCAGGGAGTCCTG
1260
a V Y L H A C V T E T L R L Y P A V P Q D -
CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAGGGCCGGCGGG
1261
GGGTTCCCCTAGGACCTCCTGCTGCACGACGGCCTGCCCTGCTTCCACTCCCGGCCGCCC
1320
a P K G I L E D D V L P D G T K V R A G G -
ATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGTACAACTGGGGCCCCGACGCG
1321
TACCACTGCATGCACGGGATGAGCTACCCCGCCTACCTCATGTTGACCCCGGGGCTGCGC
1380
a M V T Y V P Y S M G R M E Y N W G P D A -
GCGAGCTTCCGGCCGGAGCGGTGGATCAACGAGGATGGCGCGTTCCGCAACGCGTCGCCG
1381
CGCTCGAAGGCCGGCCTCGCCACCTAGTTGCTCCTACCGCGCAAGGCGTTGCGCAGCGGC
1440
a A S F R P E R W I N E D G A F R N A S P -
TTCAAGTTCACGGCGTTCCAGGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTAC
1441
AAGTTCAAGTGCCGCAAGGTCCGCCCCGGCTCCTAGACGGACCCGTTCCTGAGCCGCATG
1500
a F K F T A F Q A G P R I C L G K D S A Y -
CTGCAGATGAAGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG
1501
GACGTCTACTTCTACCGCGACCGGTAGGAGAAGGCGAAGATGTCGAAGGCCGACGACCTC
1560
a L Q M K M A L A I L F R F Y S F R L L E -

Figure 4D

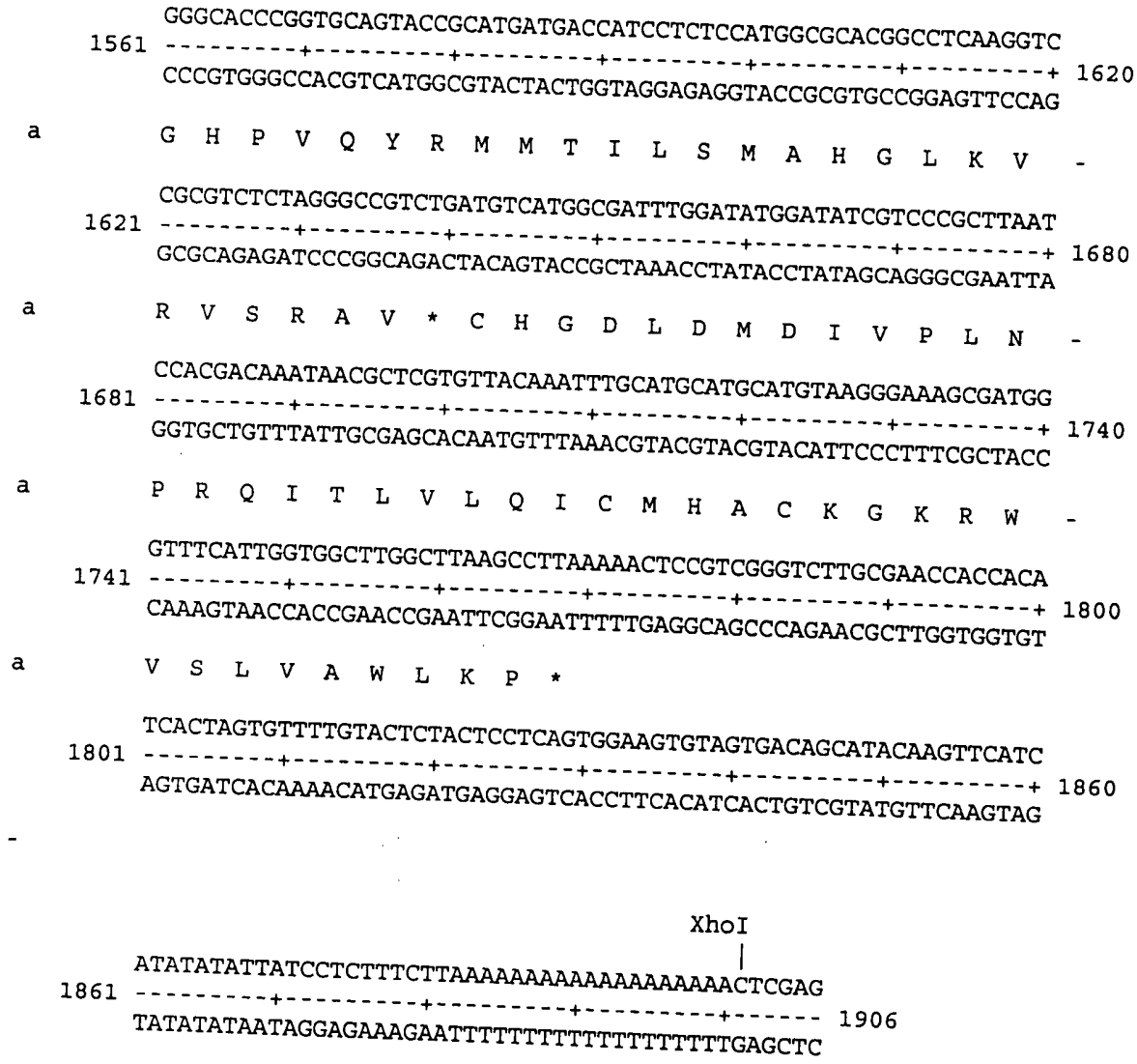

FIGURE 4D SHEET

Figure 5

```
   1  GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC
  51  GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCA GGGATGGCAA
 101  TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA
 151  GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC
 201  AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT
 251  GTCACTCCTA CTTTATTCCT TGGTTGGGCA ACTTCCAATA GGCTCATGTT
 301  AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT
 351  ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT
 401  TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA
 451  ATTTTCTCAG TTTGGTCCAT GTAATTTTTG AAGTGAGGTT CCTTAAATTT
 501  CATTATGCTT CCTTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACTT
 551  TGGGTTCACA AATTGACTCA CAAGAAAACA AATTCACTTT TGGGTTCACA
 601  AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA
 651  AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT
 701  CTTTCTGGTT GGTTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC
 751  AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT
 801  AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA
 851  GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA
 901  GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTTGG GGTCACACCA
 951  AGATTGTCTC TCTCGAGGTT GGGGGGTCCC TAAGGTTGGT AGTAGCAATA
1001  CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA
1051  TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACCAT GGAGGAAGCT
1101  CACATCACGC CGGCGACGCC ATCGCCATTC TTCCCACTAG CAGGGCCTCA
1151  CAAGTACATC GCGCTCCTCC TGGTTGTCCT CTCATGGATC CTGGTCCAGA
1201  GGTGGAGCCT GAGGAAGCAG AAAGGCCCGA GATCATGGCC AGTCATCGGT
1251  GCAACGGTGG AGCAGCTGAG GAACTACCAC CGGATGCACG ACTGGCTTGT
1301  CGGGTACCTG TCACGGCACA GGACAGTGAC CGTCGACATG CCGTTCACTT
1351  CCTACACCTA CATCGCTGAC CCGGTGAATG TCGAGCATGT CCTCAAGACT
```

FOOTAGE.NET

Figure 5B

1401 AACTTCACCA ATTACCCCAA GGTAAATGAC CTGAACTCAC TGATGTTCAG
1451 TCTTCGGAAA TCAGAGCTGA AAGCTGAATC GAATGTGCCT GAACACCGTG
1501 TAGGGAATCG TGTACAGATC CTACATGGAC GTGCTCCTCG GTGACGGCAT
1551 CTTCAACGCC GACGGCGAGC TGTGGAGGAA GCAGAGGAAG ACGGCGAGTT
1601 TCGAGTTCGC CTCCAAGAAC CTGAGGGATT TCAGCGCCAT TGTGTTCAGA
1651 GAGTACTCCC TGAAGCTGTC GGGTATACTG AGCCAGGCAT CCAAGGCAGG
1701 CAAAGTTGTG GACATGCAGG TGAGATCACT GCTCCCTTGC CATTGCCAAC
1751 ATGAGCATTT CAACCTGAGA CACGAGAGCT ACCTTGCCGA TTCAGGAACT
1801 TTACATGAGG ATGACGCTGG ACTCCATCTG CAAGGTTGGG TTCGGGGTCG
1851 AGATCGGCAC GCTGTCGCCG GATCTCCCCG AGAACAGCTT CGCGCAGGCG
1901 TTCGATGCCG CCAACATCAT CGTCACGCTG CGGTTCATCG ACCCGCTGTG
1951 GCGCATCAAG AGGTTCTTCC ACGTCGGGTC AGAGGCCCTC CTAGCGCAGA
2001 GCATCAAGCT CGTGGACGAG TTCACCTACA GCGTGATCCG CCGGAGGAAG
2051 GCCGAGATCG TCGAGGCCCG GGCCAGCGGC AAACAGGAGA AGGTACGTGC
2101 ACATGACTGT TTCGATTCTT CAGTTCATCG TCTTGGCCGG GATGGACCTG
2151 ATCCTGATTG ATTATATATC CGTGTGACTT GTGAGGACAA ATTAAAATGG
2201 GCAGATGAAG CACGACATCC TGTCACGGTT CATCGAGCTA GGCGAGGCCG
2251 GCGACGACGG CGGCGGCTTC GGGGACGACA AGAGCCTCCG GGACGTGGTG
2301 CTCAACTTCG TGATCGCCGG GCGGGACACG ACGGCGACGA CGCTGTCGTG
2351 GTTCACGCAC ATGGCCATGT CCCACCCGGA CGTGGCCGAG AAGCTGCGCC
2401 GCGAGCTGTG CGCGTTCGAG GCGGAGCGCG CGCGCGAGGA GGGCGTCGCG
2451 CTCGTGCCCT GCGGCGGCGC TGACGCCGAC GACAAGGCGT TCGCCGCCCG
2501 CGTGGCGCAG TTCGCGGGCC TCCTCACCTA CGACAGCCTC GGCAAGCTGG
2551 TCTACCTCCA CGCCTGCGTC ACCGAGACGC TCCGCCTGTA CCCCGCCGTC
2601 CCTCAGGTGA GCGCGCCCGA CACGCGACCT CCGGTCCAGA GCACAGCATG
2651 CAGTGAGTGG ACCTGAATGC AATGCACATG CACTTGCGCG CGCGCAGGAC
2701 CCCAAGGGGA TCCTGGAGGA CGACGTGCTG CCGGACGGGA CGAAGGTGAG
2751 GGCCGGCGGG ATGGTGACGT ACGTGCCCTA CTCGATGGGG CGGATGGAGT

Figure 5C

2801 ACAACTGGGG CCCCGACGCG GCGAGCTTCC GGCCGGAGCG GTGGATCAAC

2851 GAGGATGGCG CGTTCCGCAA CGCGTCGCCG TTCAAGTTCA CGGCGTTCCA

2901 GGCGGGGCCG AGGATCTGCC TGGGCAAGGA CTCGGCGTAC CTGCAGATGA

2951 AGATGGCGCT GGCCATCCTC TTGCGCTTCT ACAGCTTCCG GCTGCTGGAG

3001 GGGCACCCGG TGCAGTACCG CATGATGACC ATCCTCTCCA TGGCGCACGG

3051 CCTCAAGGTC CGCGTCTCTA GGGCCGTCTG ATGTCATGGC GATTTGGGAT

3101 ATCATCCCGC TTAATCCTTA AAAATTTGCA TGCATGCATG TAAGGGAAAG

3151 CGATGGGTTT CATTGGTGGC TTGGCTTAAG CCTTAAAAAC TCCGTCGGGT

3201 CTTGCGAACC ACCACATCAC TAGTGTTTTG TACTCTACTC CTCAGTGGAA

3251 GTGTAGTGAC AGCATACAAG TTCATCATAT ATATTATCCT CTTTCTTCGC

3301 CGGATGCTTC CCGGGACCTT TTGGAGACCA TTACTGACAG GCGTGTGAAA

3351 AAAAGGCTTC TTCTGCGGCG AAGTTTTGGG TTCAGAGTCT TGGCGTCTTT

3401 GCAGCAGAAA AAAGGTTTGG AAGGATCTGA ACCCTGAACC GAAAATGGCT

3451 TCGGAAATAT GCTCGCATCG GGGCGGGGCC GTCACTCGGG ATGACGACAA

3501 GCCCACAAGC AGTGAGAGCG AAGCGATCTT TGGAGTTTGG AGACACTCTC

3551 GGACCCCTCG GCGCTCCGCG AGCTCATCTT CGCCTCCTCT GTCGTGTCCG

3601 TGGCGGCACC GCGCCCGCCC GCCTCGTGTT CGACCAAATC CCGCGCCCCG

3651 ACCGGTTCGT GTACAACACC CTCATCCGCG GCGCCGCGCG CAGTGACACG

3701 CCCCGGGACG CCGTATACAT CTATAAATCA TGGTATTGTA CTTTATTTTC

3751 AAACGGCCTT AACACAACCA TATTTTTATG GTAAACACGT TCAAAATTGA

3801 CACAAATTTA AAACAGGCAC AAACCGTAGC TAAACATAAG AGAATGAGAG

3851 ACAACCCAAA GGTTAGAGAT GAAATAAGCT GAGTAAACGA CGAATTC

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Figure 6

```
1051 TCCATCACTTGTAGACTGGACCCTTCATCAAGAGCACCATGGAGGAAGCT 1100
                                      |    |  || |  |||||||
   1 .............................GAATTCGGCACGAGGGAAGCT 21

1101 CACATCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 1150
     ||| ||||||||||||||||||||||||||||||||||||||||||||||
  22 CACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 71

1151 CAAGTACATCGCGCTCCTCCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 1200
     |||||||||||||||||| |||||||||||||||||||||||||||||||
  72 CAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 121

1201 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGT 1250
     |||||||||||||||||||||||||||||||||||||||||||||||||
 122 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGC 171

1251 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 172 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 221

1301 CGGGTACCTGTCACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 222 CGGGTACCTGTCACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 271

1351 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 1400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 272 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 321

1401 AACTTCACCAATTACCCCAAGGTAAATGACCTGAACTCACTGATGTTCAG 1450
     ||||||||||||||||||
 322 AACTTCACCAATTACCCCA............................... 340

                              .
                              .
                              .

1501 TAGGGAATCGTGTACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 1550
      |||||||||||||||||||||||||||||||||||||||||||||||||
 341 .AGGGAATCGTGTACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 389

1551 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 1600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 390 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 439

1601 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTCAGCGCCATTGTGTTCAGA 1650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 440 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTCAGCGCCATTGTGTTCAGA 489

1651 GAGTACTCCCTGAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGG 1700
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 490 GAGTACTCCCTGAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGG 539

1701 CAAAGTTGTGGACATGCAGGTGAGATCACTGCTCCCTTGCCATTGCCAAC 1750
     ||||||||||||||||
 540 CAAAGTTGTGGACATG.................................. 555
```

Figure 6B

```
                .         .         .         .         .
1751 ATGAGCATTTCAACCTGAGACACGAGAGCTACCTTGCCGATTCAGGAACT 1800
                                               ||||||||
 556 ..........................................CAGGAACT 563

                .         .         .         .         .
1801 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCGGGGTCG 1850
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 564 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCGGGGTCG 613

                .         .         .         .         .
1851 AGATCGGCACGCTGTCGCCGGATCTCCCCGAGAACAGCTTCGCGCAGGCG 1900
     |||||||||||||||||| |||||||||||||||||||||||||||||||
 614 AGATCGGCACGCTGTCGCCAGATCTCCCCGAGAACAGCTTCGCGCAGGCG 663

                .         .         .         .         .
1901 TTCGATGCCGCCAACATCATCGTCACGCTGCGGTTCATCGACCCGCTGTG 1950
     ||||||||||||||||||||| ||||||||||||||||||||||||||||
 664 TTCGATGCCGCCAACATCATCATCACGCTGCGGTTCATCGACCCGCTGTG 713

                .         .         .         .         .
1951 GCGCATCAAGAGGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGA 2000
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 714 GCGCATCAAGAGGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGA 763

                .         .         .         .         .
2001 GCATCAAGCTCGTGGACGAGTTCACCTACAGCGTGATCCGCCGGAGGAAG 2050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 764 GCATCAAGCTCGTGGACGAGTTCACCTACAGCGTGATCCGCCGGAGGAAG 813

                .         .         .         .         .
2051 GCCGAGATCGTCGAGGCCCGGGCCAGCGGCAAACAGGAGAAGGTACGTGC 2100
     |||||||||||||||| |||||||||||||||||||||||
 814 GCCGAGATCGTCGAGGTCCGGGCCAGCGGCAAACAGGAGA.......... 853

                          .
                          .
                          .

                .         .         .         .         .
2201 GCAGATGAAGCACGACATCCTGTCACGGTTCATCGAGCTAGGCGAGGCCG 2250
       ||||||||||||||||||||||||||||||||||||| ||||||||||
 854 ..AGATGAAGCACGACATCCTGTCACGGTTCATCGAGCTGGGCGAGGCCG 901

                .         .         .         .         .
2251 GCGACGACGGCGGCGGCTTCGGGGACGACAAGAGCCTCCGGGACGTGGTG 2300
     |||||||||||||||||||||||||||| |||||||||||||||||||||
 902 GCGACGACGGCGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTG 951

                .         .         .         .         .
2301 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCGTG 2350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 952 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCGTG 1001

                .         .         .         .         .
2351 GTTCACGCACATGGCCATGTCCCACCCGGACGTGGCCGAGAAGCTGCGCC 2400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1002 GTTCACGCACATGGCCATGTCCCACCCGGACGTGGCCGAGAAGCTGCGCC 1051

                .         .         .         .         .
2401 GCGAGCTGTGCGCGTTCGAGGCGGAGCGCGCGCGCGAGGAGGGCGTCGCG 2450
     |||||||||||||||||||||||||||||||||||||||||||||| |||
1052 GCGAGCTGTGCGCGTTCGAGGCGGAGCGCGCGCGCGAGGAGGGCGTCACG 1101

                .         .         .         .         .
2451 CTCGTGCCCTGCGGCGGCGCTGACGCCGACGACAAGGCGTTCGCCGCCCG 2500
     ||||||| ||||||||||||||||||||||||||||||||||||||||||
1102 CTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCGTTCGCCGCCCG 1151
```

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Figure 6C

```
2501 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 2550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1152 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 1201

2551 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 2600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1202 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 1251

2601 CCTCAGGTGAGCGCGCCCGACACGCGACCTCCGGTCCAGAGCACAGCATG 2650
     |||
1252 CCT..................................................  1254

2651 CAGTGAGTGGACCTGAATGCAATGCACATGCACTTGCGCGCGCGCAGGAC 2700
                                                  ||||||
1255 .....................................................CAGGAC 1260

2701 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 2750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1261 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 1310

2751 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 2800
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1311 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 1360

2801 ACAACTGGGGCCCCGACGCGGCGAGCTTCCGGCCGGAGCGGTGGATCAAC 2850
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1361 ACAACTGGGGCCCCGACGCGGCGAGCTTCCGGCCGGAGCGGTGGATCAAC 1410

2851 GAGGATGGCGCGTTCCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 2900
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1411 GAGGATGGCGCGTTCCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 1460

2901 GGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 2950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1461 GGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 1510

2951 AGATGGCGCTGGCCATCCTCTTGCGCTTCTACAGCTTCCGGCTGCTGGAG 3000
     |||||||||||||||||||| ||||||||||||||||||||||||||||
1511 AGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG 1560

3001 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 3050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 1610

3051 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTG.... 3096
     ||||||||||||||||||||||||||||||||||||||||||||||||
1611 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATA 1660

3097 .GGATATCATCCCGCTTAATCC.....................TTAAAAATT 3126
     |||||||  ||||||||||||                  |||  |||||
1661 TGGATATCGTCCCGCTTAATCCACGACAAATAACGCTCGTGTTACAAATT 1710

3127 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 3176
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1711 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 1760
```

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Figure 6D

```
3177 TAAGCCTTAAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 3226
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1761 TAAGCCTTAAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 1810

3227 TTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC 3276
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1811 TTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC 1860

3277 ATATATATTATCCTCTTTCTTCGCCGGATGCTTCCCGGACCTTTTGGAG 3326
     |||||||||||||||||||||      |           ||
1861 ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAAACTCGAG.... 1906
                             .
                             .
                             .
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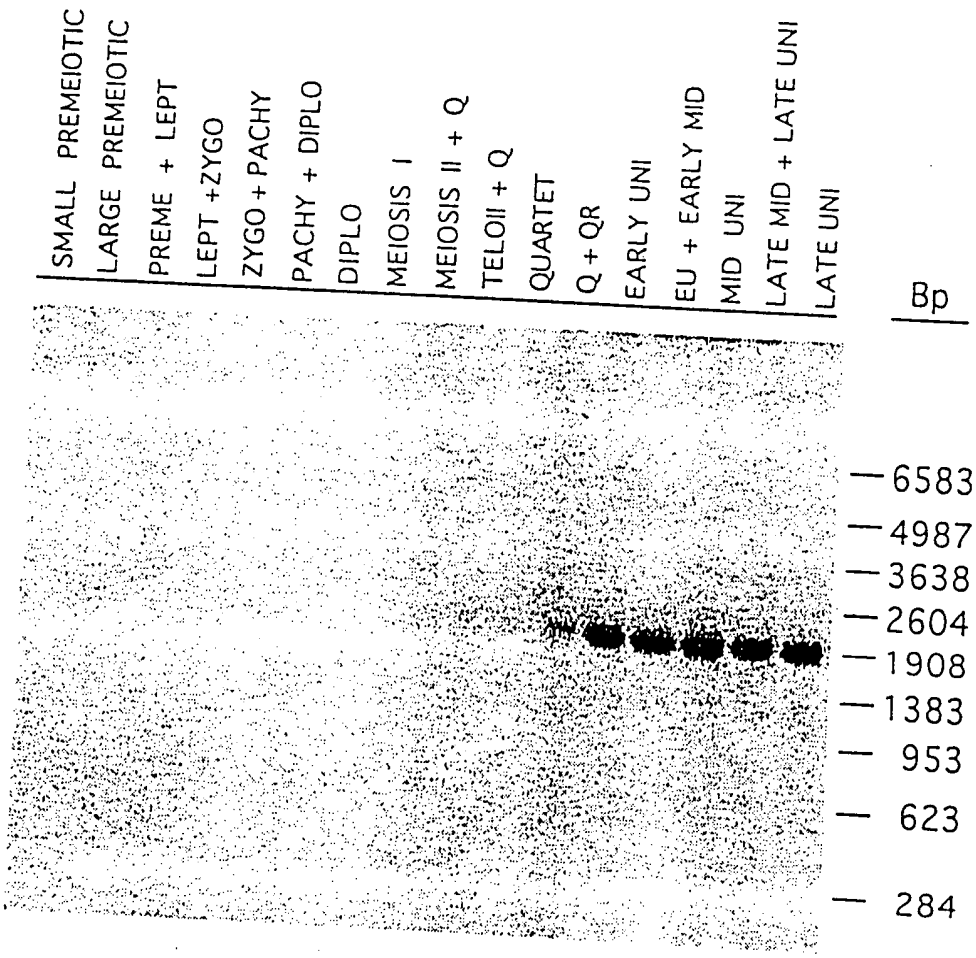
SMALL PREMEIOTIC
LARGE PREMEIOTIC
PREME + LEPT
LEPT +ZYGO
ZYGO + PACHY
PACHY + DIPLO
DIPLO
MEIOSIS I
MEIOSIS II + Q
TELOII + Q
QUARTET
Q + QR
EARLY UNI
EU + EARLY MID
MID UNI
LATE MID + LATE UNI
LATE UNI
Bp
6583
4987
3638
2604
1908
1383
953
623
284

Figure 7

Figure 8

1 GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC

51 GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCA GGGATGGCAA

101 TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA

151 GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC

201 AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT

251 GTCACTCCTA CTTTATTCCT TGGTTGGGCA ACTTCCAATA GGCTCATGTT

301 AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT

351 ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT

401 TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA

451 ATTTTCTCAG TTTGGTCCAT GTAATTTTTG AAGTGAGGTT CCTTAAATTT

501 CATTATGCTT CCTTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACTT

551 TGGGTTCACA AATTGACTCA CAAGAAAACA AATTCACTTT TGGGTTCACA

601 AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA

651 AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT

701 CTTTCTGGTT GGTTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC

751 AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT

801 AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA

851 GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA

901 GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTTGG GGTCACACCA

951 AGATTGTCTC TCTCGAGGTT GGGGGGTCCC TAAGGTTGGT AGTAGCAATA

1001 CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA

1051 TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACC**AT** **GG**

10021657.121401

SBMu200 Promoter Analysis: 5' Deletions

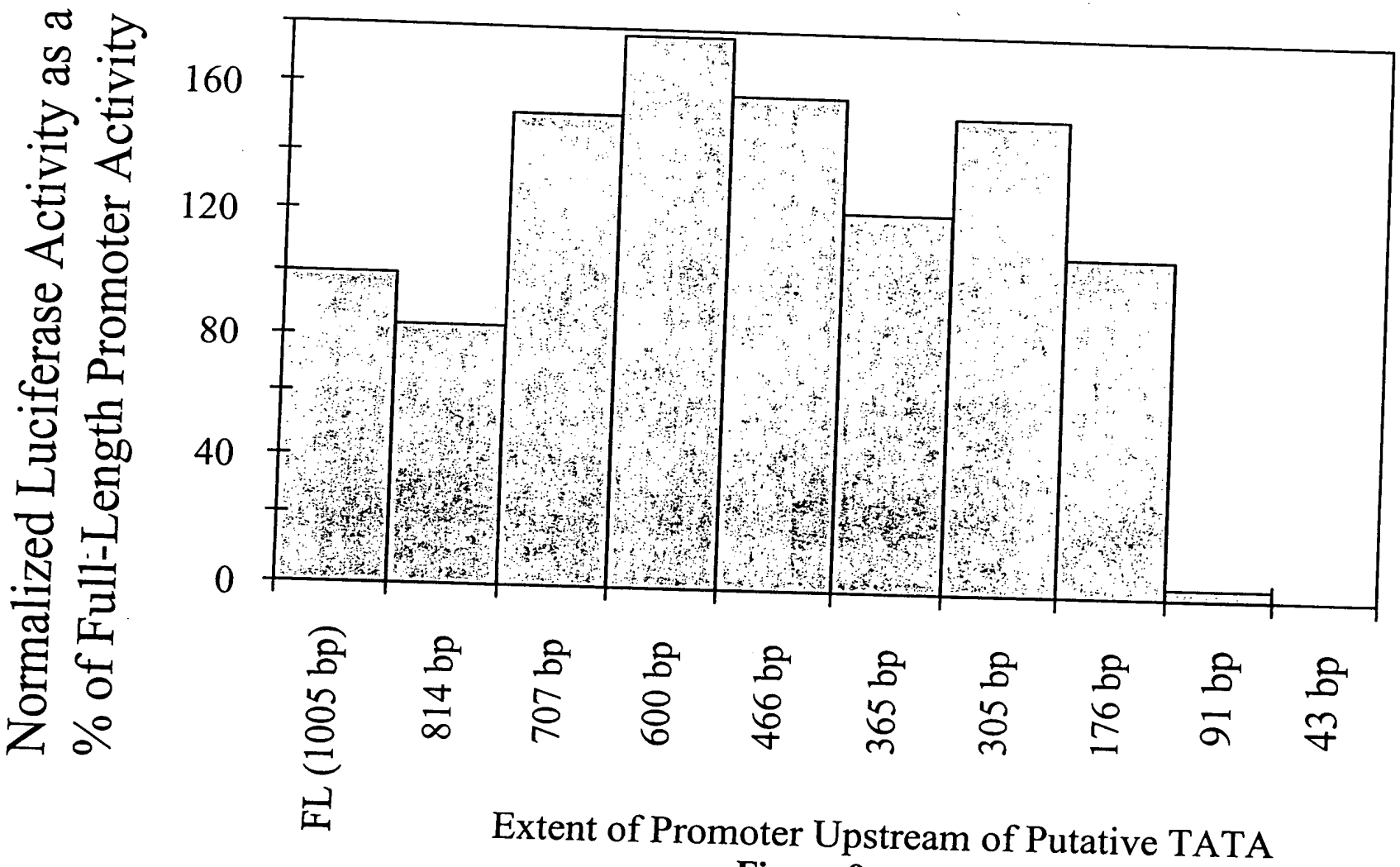

Figure 9

SBMu200 "Minimal" Promoter

```
-180 CCCCATCTCA TTTTCTTGGT TGGCAGATCA CAAAAAGGAA CACAAAGGCT
       LS01   |   LS02   |   LS03   |   LS04   |   LS05   |
-130 AAGCCTCCTA CTTGTTCGGG AGTTAGGTCA GGGACACCAT ATGAATGAAA
       LS06   |   LS07   |   LS08   |   LS09   |   LS10   |
 -80 GAAATCTTAA TTTGGGGTCA CACCAAGATT GTCTCTCTCG AGGTTGGGGG
       LS11   |   LS12   |   LS13   |   LS14   |   LS15   |
 -30 GTCCCTAAGG TTGGTAGTAG CAATACCCAA TATATCACCT AACAAACCCA
       LS16   |   LS17   |   LS18   |

  20 ATCCATGCTA CATACATACA TAGCATCCAT CACTTGTAGA CTGGACCCTT

  70 CATCAAGAGC ACCATGG
```

Coordinates are relative to the putative TATA box (underlined). P motifs are in italic.
[ ] = Del -176/-92 [ ] = Del -89/-44 [ ] = Del -39/-8
Linker scanning mutations that reduce activity to ~5% or less are in bold. Mutations with a significant but less pronounced effect are in bold italic.

Figure 10

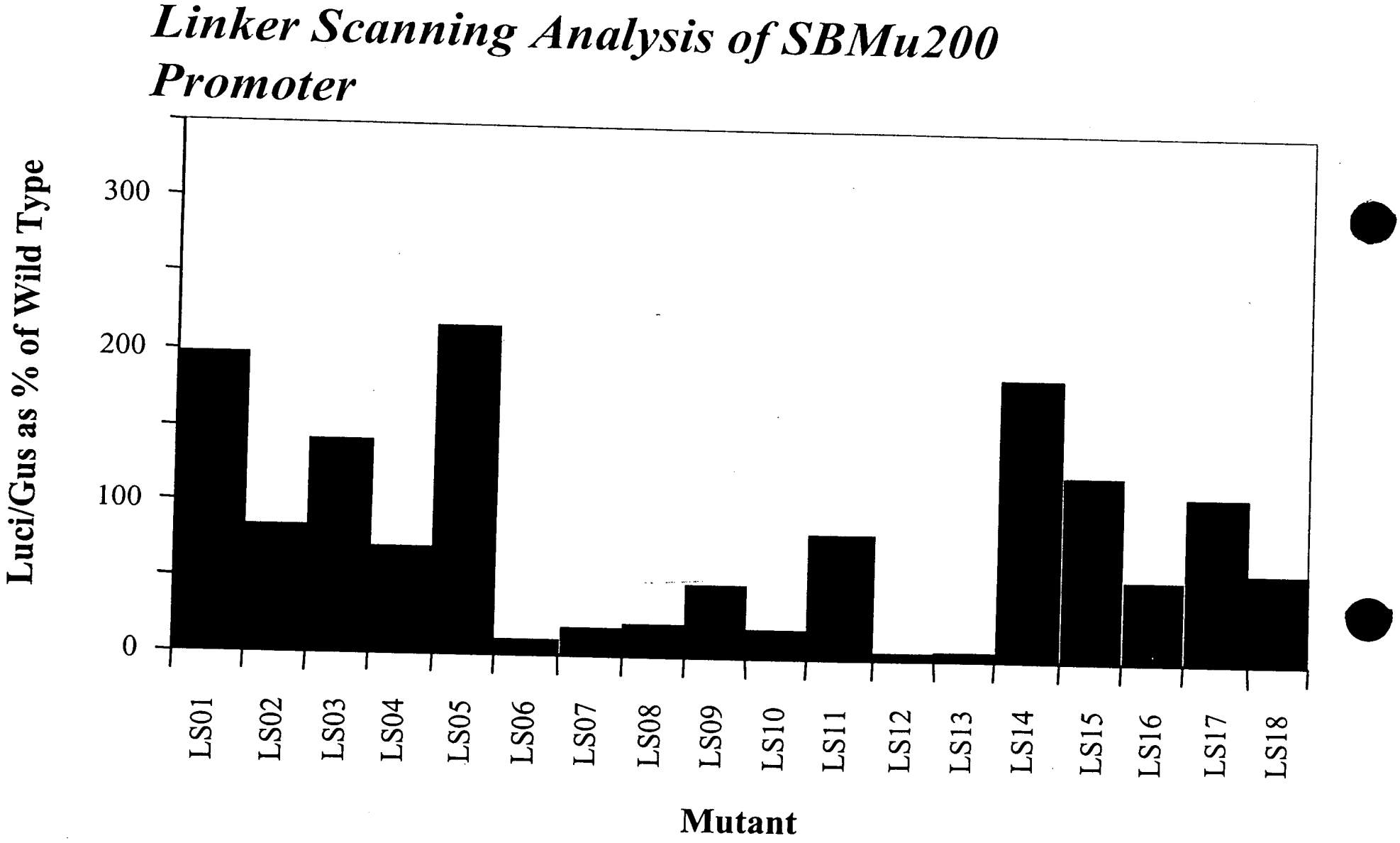
Linker Scanning Analysis of SBMu200 Promoter
Luci/Gus as % of Wild Type
300
200
100
0
LS01
LS02
LS03
LS04
LS05
LS06
LS07
LS08
LS09
LS10
LS11
LS12
LS13
LS14
LS15
LS16
LS17
LS18
Mutant

Figure 11

Figure 12

```
   1 ..............................................GGAA 4
                                                    |  |
 201 CCGGATGCACGACTGGCTTGTCGGGTACCTGTCACGGCACAGGACAGTGA 250
              .         .         .         .         .
   5 TTCGGCTTATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT 54
             ||||||||||||||||||||||||||||||||||||||||||
 251 CCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT 300
              .         .         .         .         .
  55 GTCGAGCATGTCCTCAAGACTAACTTCACCAATTACCCCAAGGGGGACGT 104
     ||||||||||||||||||||||||||||||||||||||||||||   |||
 301 GTCGAGCATGTCCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGT 350
              .         .         .         .         .
 105 GTACAGATCCTACATGGATGTGCTCCTCGGTGACGGCATATTCAACGCTG 154
     |||||||||||||||||| |||||||||||||||||||| |||||||| |
 351 GTACAGATCCTACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCG 400
              .         .         .         .         .
 155 ACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTTTCGAGTTCGCC 204
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 ACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTTTCGAGTTCGCC 450
              .         .         .         .         .
 205 TCCAAGAACCTGAGGGATTTCAGTGCCAATGTTTTCAGAGAGTACTCCCT 254
     ||||||||||||||||||||||| |||| ||| |||||||||||||||||
 451 TCCAAGAACCTGAGGGATTTCAGCGCCATTGTGTTCAGAGAGTACTCCCT 500
              .         .         .         .         .
 255 GAAGCTGTCGGGCATACTGAGTCAGGCATCCAAGGCAGGCAAAGTTGTTG 304
     |||||||||||| |||||||| |||||||||||||||||||||||||| |
 501 GAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGGCAAAGTTGTGG 550
              .         .         .         .         .
 305 ACATGCAGGAACTTTACATGAGGATGACACTGGACTCGATCTGCAANGTT 354
     |||||||||||||||||||||||||||| |||||||| ||||||||:|||
 551 ACATGCAGGAACTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT 600
              .         .         .         .         .
 355 GGGTTCGGGGTCNANATCGGCACGCTGTCNCCGGATCTCCCCGAGAACAG 404
     ||||||||||||:|:||||||||||||||:|| |||||||||||||||||
 601 GGGTTCGGGGTCGAGATCGGCACGCTGTCGCCAGATCTCCCCGAGAACAG 650
              .         .         .         .         .
 405 CTTCNCCCAAGCGTTCGATGCCGCTAACATCATCGTCACNCTGCGGTTCA 454
     ||||:| || |||||||||||||| ||||||||| ||||:||||||||||
 651 CTTCGCGCAGGCGTTCGATGCCGCCAACATCATCATCACGCTGCGGTTCA 700
              .         .         .         .         .
 455 TCCACCCNCTGTGGCGCATCCAGAAGTTCTTCCCCNGTCA.......... 494
     || ||||:|||||||||||| ||| |||||||| |:
 701 TCGACCCGCTGTGGCGCATCAAGAGGTTCTTCCACGTCGGTCAGAGGCC 750
```

Percent Similarity: 92.510 Percent Identity: 90.891
Sb200-Sorghr.Pep x Sb20081.Pep February 13, 1997 11:29 ..

```
              .         .         .         .         .
   5 MPFTSYTYIADPVNVEHVLKTNFTNYPKGDVYRSYMDVLLGDGIFNADGE 54
     ||||||||||||||||||||||||||||| ||||||||||||||||||||
  87 MPFTSYTYIADPVNVEHVLKTNFTNYPKGIVYRSYMDVLLGDGIFNADGE 136
              .         .         .         .         .
  55 LWRKQRKTASFEFASKNLRDFSANVFREYSLKLSGILSQASKAGKVVDMQ 104
     ||||||||||||||||||||||| ||||||||||||||||||||||||||
 137 LWRKQRKTASFEFASKNLRDFSAIVFREYSLKLSGILSQASKAGKVVDMQ 186
```

10021657.121401

Figure 12B

```
                 .         .         .         .         .
105 ELYMRMTLDSICXVGFGVXIGTLSPDLPENSFXQAFDAANIIVTLRFIHP 154
    |||||||||||| ||||| ||||||||||||| |||||||||:|||||.|
187 ELYMRMTLDSICKVGFGVEIGTLSPDLPENSFAQAFDAANIIITLRFIDP 236

155 LWRIQKFF 162
    ||||.:||
237 LWRIKRFF 244
```

10021657.121401